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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,123

DATE: 12/21/2001
TIME: 12:47:50

Input Set : A:\001560-397.ST25.txt
Output Set: N:\CRF3\12212001\I830123.raw

4 <110> APPLICANT: Iida, Shigeru
 5 Tanaka, Sachiko
 6 Inagaki, Yoshishige
 8 <120> TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
 10 <130> FILE REFERENCE: 001560-397
 12 <140> CURRENT APPLICATION NUMBER: 09/830,123
 13 <141> CURRENT FILING DATE: 2001-04-24
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05722
 16 <151> PRIOR FILING DATE: 2000-08-24
 18 <150> PRIOR APPLICATION NUMBER: JP 11/236800
 19 <151> PRIOR FILING DATE: 1999-08-24
 21 <160> NUMBER OF SEQ ID NOS: 20
 23 <170> SOFTWARE: PatentIn version 3.1

**Does Not Comply
 Corrected Diskette Needed**

ERRORED SEQUENCES

196 <210> SEQ ID NO: 2
 197 <211> LENGTH: 542
 198 <212> TYPE: PRT
 199 <213> ORGANISM: Ipomea nil
 201 <220> FEATURE:
 202 <221> NAME/KEY: peptide
 203 <222> LOCATION: (1)..(542)
 204 <223> OTHER INFORMATION: Amino acid sequence of protein regulating the pH of vacuoles
 207 <400> SEQUENCE: 2
 209 Met Ala Phe Gly Leu Ser Ser Leu Leu Gln Asn Ser Asp Leu Phe Thr
 210 1 5 10 15
 212 Ser Asp His Ala Ser Val Val Ser Met Asn Leu Phe Val Ala Leu Leu
 213 20 25 30
 215 Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
 216 35 40 45
 218 Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
 219 50 55 60
 221 Ile Leu Leu Leu Ser Gly Gly Lys Ser Ser His Leu Leu Val Phe Ser
 222 65 70 75 80
 224 Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
 225 85 90 95
 227 Gly Phe Gln Val Lys Lys Gln Phe Phe Val Asn Phe Met Thr Ile
 228 100 105 110
 230 Met Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Cys Ser Ile Ile Ser
 231 115 120 125
 233 Phe Gly Ala Val Lys Ile Phe Lys His Leu Asp Ile Asp Phe Leu Asp
 234 130 135 140
 236 Phe Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser
 237 145 150 155 160
 239 Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Leu Leu Tyr

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240	165	170	175
242 Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val			
243	180	185	190
245 Leu Phe Asn Ala Ile Gln Ser Phe Asp Met Thr Ser Phe Asp Pro Lys			
246	195	200	205
248 Ile Gly Leu His Phe Ile Gly Asn Phe Leu Tyr Leu Phe Leu Ser Ser			
249	210	215	220
251 Thr Phe Leu Gly Val Gly Ile Gly Leu Leu Cys Ala Tyr Ile Ile Lys			
252	225	230	235
254 Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met			
255	245	250	255
257 Met Leu Met Ser Tyr Leu Ser Tyr Ile Met Ala Glu Leu Phe Tyr Leu			
258	260	265	270
260 Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr			
261	275	280	285
263 Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Arg His Ser			
E--> 264	290	295	300 300
266 Phe Ala Thr Leu Ser Phe Val Ala Glu Thr Phe Ile Phe Leu Tyr Val			
267	305	310	315
269 Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Lys Asn Ser			
270	325	330	335
272 Gln Gly Leu Ser Val Ala Val Ser Ser Ile Leu Val Gly Leu Ile Leu			
273	340	345	350
275 Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu			
276	355	360	365
278 Ala Lys Lys Asn Ser Ser Asp Lys Ile Ser Phe Arg Gln Gln Ile Ile			
279	370	375	380
281 Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala			
282	385	390	395
284 Tyr Asn Lys Phe Thr Thr Ser Gly His Thr Ser Leu His Glu Asn Ala			
285	405	410	415
287 Ile Met Ile Thr Ser Thr Val Thr Val Val Leu Phe Ser Thr Val Val			
288	420	425	430
290 Phe Gly Leu Met Thr Lys Pro Leu Ile Asn Leu Leu Pro Pro His			
291	435	440	445
293 Lys Gln Met Pro Ser Gly His Ser Ser Met Thr Thr Ser Glu Pro Ser			
294	450	455	460
296 Ser Pro Lys His Phe Thr Val Pro Leu Leu Asp Asn Gln Pro Asp Ser			
297	465	470	475
299 Glu Ser Asp Met Ile Thr Gly Pro Glu Val Ala Arg Pro Thr Ala Leu			
300	485	490	495
302 Arg Met Leu Leu Arg Thr Pro Thr His Thr Val His Arg Tyr Trp Arg			
303	500	505	510
305 Lys Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe			
306	515	520	525
308 Val Pro Phe Val Ala Gly Ser Pro Val Glu Gln Ser Pro Arg			
309	530	535	540
938 <210> SEQ ID NO: 17			
939 <211> LENGTH: 553			

RAW SEQUENCE LISTING
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940 <212> TYPE: PRT
941 <213> ORGANISM: Nierembergia hybrida
943 <220> FEATURE:
944 <221> NAME/KEY: peptide
945 <222> LOCATION: (1)..(553)
946 <223> OTHER INFORMATION: Amino acid sequence of protein regulating the pH of vacuoles
948 <400> SEQUENCE: 17
950 Met Ala Phe Asp Phe Gly Thr Leu Leu Gly Lys Met Asn Asn Leu Thr
951           5          10          15
953 Thr Ser Asp His Gln Ser Val Val Ser Val Asn Leu Phe Val Ala Leu
954           20         25          30
956 Ile Cys Ala Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp
957           35         40          45
959 Met Asn Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Val
960           50         55          60
962 Ile Ile Leu Leu Ile Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe
963   65        70          75          80
965 Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn
966           85         90          95
968 Ala Gly Phe Gln Val Lys Lys Lys Ser Phe Phe Arg Asn Phe Ser Thr
969           100        105         110
971 Ile Met Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Ile Ile Ile
972           115        120         125
974 Ser Ala Gly Ala Ile Gly Ile Phe Lys Lys Met Asp Ile Gly His Leu
975           130        135         140
977 Glu Ile Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp
978   145        150         155         160
980 Ser Val Cys Thr Leu Gln Val Leu Asn Gln Glu Glu Thr Pro Leu Leu
981           165        170         175
984 Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val
985           180        185         190
987 Val Leu Phe Asn Ala Val Gln Asn Phe Asp Leu Ser His Ile Ser Thr
988           195        200         205
990 Gly Lys Ala Leu Gln Leu Ile Gly Asn Phe Leu Tyr Leu Phe Ala Ser
991           210        215         220
993 Ser Thr Phe Leu Gly Val Ala Val Gly Leu Leu Ser Ala Phe Ile Ile
994   225        230         235         240
996 Lys Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Ile
997           245        250         255
999 Met Ile Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Tyr
1000          260        265         270
1002 Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His
1003          275        280         285
1005 Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His
1006          290        295         300
1008 Thr Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Ile Phe Leu Tyr
1009   305        310         315         320
1011 Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Ser Asp
1012          325        330         335

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1014 Ser Pro Gly Thr Ser Ile Lys Val Ser Ser Ile Leu Leu Gly Leu Val
1015 340 345 350
1017 Leu Val Gly Arg Gly Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn
1018 355 360 365
1020 Leu Thr Lys Lys Asn Pro Glu Asp Lys Ile Ser Phe Asn Gln Gln Val
1021 370 375 380
1023 Thr Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu
1024 385 390 395 400
1026 Ala Tyr Asn Gln Phe Thr Arg Gly Gly His Thr Gln Leu Arg Ala Asn
1027 405 410 415
1029 Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Val
1030 420 425 430
1032 Val Phe Gly Leu Met Thr Lys Pro Leu Ile Leu Leu Leu Pro Ser
1033 435 440 445
1035 Gln Lys His Leu Ile Arg Met Ile Ser Ser Glu Pro Met Thr Pro Lys
1036 450 455 460
1038 Ser Phe Ile Val Pro Leu Leu Asp Ser Thr Gln Asp Ser Glu Ala Asp
E--> 1039 465 470→ 475→ 480→
1041 Leu Gly Arg His Val Pro Arg Pro His Ser Leu Arg Met Leu Leu Ser
E--> 1042 485 490 495
1044 Thr Pro Ser His Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asn Ala
E--> 1045 500 505 510
1047 Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro
E--> 1048 515 520 525
1050 Gly Ser Pro Thr Glu Pro Val Glu Pro Thr Glu Pro Arg Pro Ala Glu
E--> 1051 530 535 540
1053 Ser Arg Pro Thr Glu Pro Thr Asp Glu
E--> 1054 545 550

VERIFICATION SUMMARY
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Input Set : A:\001560-397.ST25.txt
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L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:264 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:610 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:618 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:839 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:891 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:895 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:899 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:903 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:907 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

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Input Set : A:\001560-397.ST25.txt
Output Set: N:\CRF3\12212001\I830123.raw

L:911 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:915 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:919 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:1039 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17
L:1087 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18